

L Number	Hits	Search Text	DB	Time stamp
1	2	5955309.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/08/31 11:04
2	2	5874243.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/08/31 11:05
3	2	6043054.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/08/31 11:05
4	2	5976834.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/08/31 11:06
5	2	5955308.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/08/31 11:06
6	2	6048711.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/08/31 11:06
-	2	6262246.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/08/31 11:04
-	13	gerald-christophe-p-g.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/10/01 12:40
-	38	jones-kenneth-a.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/10/01 12:40
-	19	bonini-james-a.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/10/01 12:41
-	16	borowsky-beth.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/10/01 12:41
-	13	npff adj receptor	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/10/01 12:41

09866248 Results

SEQ ID NO: 6

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	2208	100.0	420	2	AAW81358	Aaw81358 Human 7-t
2	2208	100.0	420	3	AAY79375	Aay79375 Human neu
3	2208	100.0	420	3	AAY99930	Aay99930 HLWAR77 p
4	2208	100.0	420	4	AAU00233	Aau00233 Orphan re
5	2208	100.0	420	5	AAU79013	Aau79013 Human G p
6	2208	100.0	522	4	ABB11723	Abb11723 Human GPC
7	2208	100.0	522	7	ADC89684	Adc89684 Human neu
8	2204	99.8	420	3	AAB07426	Aab07426 Amino aci
9	2204	99.8	522	4	AAU00234	Aau00234 Orphan re
10	2204	99.8	522	6	ABG73522	Abg73522 Human G-p
11	2204	99.8	522	6	ABP82012	Abp82012 Human neu
12	2115	95.8	408	3	AAY76882	Aay76882 Human NPY
13	1730.5	78.4	417	3	AAY79377	Aay79377 Rat neuro
14	1719	77.9	332	4	AAU18133	Aau18133 Novel hum
15	1719	77.9	332	4	AAU18688	Aau18688 Renal and
16	1719	77.9	332	4	AAU21718	Aau21718 Novel hum

Result No.	Score	Query					Description
		Match	Length	DB	ID		
1	2208	100.0	420	3	US-09-255-368-6	-	Sequence 6, Appli
2	1060	48.0	430	3	US-09-255-368-8	-	Sequence 8, Appli
3	1024	46.4	432	3	US-09-255-368-2	-	Sequence 2, Appli
4	525.5	23.8	444	3	US-09-119-788-2	-	Sequence 2, Appli
5	525.5	23.8	444	4	US-09-426-290-2	-	Sequence 2, Appli
6	499.5	22.6	402	3	US-08-846-704-4	-	Sequence 4, Appli
7	499.5	22.6	402	4	US-08-462-509B-2	-	Sequence 2, Appli
8	499.5	22.6	402	5	PCT-US95-05616-2	-	Sequence 2, Appli
9	499.5	22.6	425	3	US-08-846-704-2	-	Sequence 2, Appli
10	499.5	22.6	425	4	US-09-479-128-2	-	Sequence 2, Appli
11	499.5	22.6	425	4	US-09-211-823C-22	-	Sequence 22, Appli
12	476.5	21.6	369	4	US-08-462-509B-4	-	Sequence 4, Appli

RESULT 1

US-09-255-368-6
; Sequence 6, Application US/09255368
; Patent No. 6262246
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: 1795/57155-A
; CURRENT APPLICATION NUMBER: US/09/255,368
; CURRENT FILING DATE: 1999-02-22
; EARLIER APPLICATION NUMBER: 09/161,113
; EARLIER FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 6
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens

Db 1 MNEKWDTNSSENWHPIWNVNDTKHHLYSDINITYVNYYLHQHQVAAIFIISYFLIFFLCM 60
 Qy 61 MGNTVVCFIVMRNKHMHVTNLFILNLAISDLLVGIFCMPITLLDNIIAGWPFGNTMCKI 120
 |||||||
 Db 61 MGNTVVCFIVMRNKHMHVTNLFILNLAISDLLVGIFCMPITLLDNIIAGWPFGNTMCKI 120
 |||||||
 Qy 121 SGLVQGISVAASVFTLVAIAVDRFQCVVYPFKPKLTIKTAFVIIMIIWVLAITIMSPSAV 180
 |||||||
 Db 121 SGLVQGISVAASVFTLVAIAVDRFQCVVYPFKPKLTIKTAFVIIMIIWVLAITIMSPSAV 180
 |||||||
 Qy 181 MLHVQEEKYYRVRLNSQNKTSPVYWCREDWPNCMRKIYTTVLFANIYLAPLSLIVIMYG 240
 |||||||
 Db 181 MLHVQEEKYYRVRLNSQNKTSPVYWCREDWPNCMRKIYTTVLFANIYLAPLSLIVIMYG 240
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 Qy 241 RIGISLFRAAVPHTGRKNQEWHVVSRRKKQKIIKMLLIVALLFILSWLPLWTLMMLSDYA 300
 |||||||
 Db 241 RIGISLFRAAVPHTGRKNQEWHVVSRRKKQKIIKMLLIVALLFILSWLPLWTLMMLSDYA 300
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 Qy 301 DLSPNELQIINIYIYPFAHWAFLGNSSVNPIIYGFFNENFRRGFQEAFLQLCQKRAKPM 360
 |||||||
 Db 301 DLSPNELQIINIYIYPFAHWAFLGNSSVNPIIYGFFNENFRRGFQEAFLQLCQKRAKPM 360
 |||||||
 Qy 361 EAYALKAKSHVLINTSNQLVQESTFQNPNGETLLYRKAEPQQELVMEELKETTNSEI 420
 |||||||
 Db 361 EAYALKAKSHVLINTSNQLVQESTFQNPNGETLLYRKAEPQQELVMEELKETTNSEI

SUMMARIES

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Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	485.5	22.0	449	2	A41738	neuropeptide Y rec
2	480	21.7	423	2	B40470	glucocorticoid-ind
3	465	21.1	381	2	I39187	neuropeptide Y/pep
4	460	20.8	443	2	D40470	glucocorticoid-ind
5	445.5	20.2	444	2	A42685	cholecystokinin re
6	444.5	20.1	384	2	A45490	neuropeptide Y/pep
7	444	20.1	382	2	B46133	neuropeptide Y/pep
8	443.5	20.1	349	2	S12863	G protein-coupled
9	443	20.1	428	2	JN0692	cholecystokinin ty
10	437	19.8	382	2	S27388	neuropeptide Y rec
11	437	19.8	491	2	C40470	glucocorticoid-ind
12	436	19.7	436	2	JC5599	cholecystokinin-A
13	435	19.7	370	1	I52315	G protein-coupled

RESULT 1

A41738

neuropeptide Y receptor - fruit fly (*Drosophila melanogaster*)

N;Alternate names: G protein-coupled receptor PR4

C;Species: *Drosophila melanogaster*

C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 20-Apr-2000

C;Accession: A41738

R;Li, X.J.; Wu, Y.N.; North, R.A.; Forte, M.

J. Biol. Chem. 267, 9-12, 1992

A;Title: Cloning, functional expression, and developmental regulation of a neuropeptide Y receptor from *Drosophila melanogaster*.

A;Reference number: A41738; MUID:92112730; PMID:1370455

A;Accession: A41738

A;Molecule type: mRNA

A;Residues: 1-449 <LIA>

A;Cross-references: GB:M81490; NID:g157996; PIDN:AAA28727.1; PID:g157997

C;Genetics:

A;Gene: FlyBase:NepYr

A;Cross-references: FlyBase:FBgn0004842

C;Superfamily: neuropeptide Y receptor

C;Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 22.0%; Score 485.5; DB 2; Length 449;
 Best Local Similarity 34.3%; Pred. No. 1.4e-32;

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
<hr/>						
1	2208	100.0	522	1	NFF2_HUMAN	Q9y5x5 homo sapien
2	1730.5	78.4	417	1	NFF2_RAT	Q9eqd2 rattus norv
3	1060	48.0	430	1	NFF1_HUMAN	Q9gzq6 homo sapien

RESULT 1

NFF2_HUMAN
ID NFF2_HUMAN STANDARD; PRT; 522 AA.
AC Q9Y5X5; Q96RV1; Q9NR49;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neuropeptide FF receptor 2 (Neuropeptide G protein-coupled receptor)
(G-protein-coupled receptor HLWAR77).
GN GPR74 OR NPGPR OR NPFF2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RC TISSUE=Fetal;
RX MEDLINE=99180505; PubMed=10079187;
RA Cikos S., Gregor P., Koppel J.;
RT "Sequence and tissue distribution of a novel G-protein-coupled
RT receptor expressed prominently in human placenta.";
RL Biochem. Biophys. Res. Commun. 256:352-356 (1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20408933; PubMed=10851242;
RA Elshourbagy N.A., Ames R.S., Fitzgerald L.R., Foley J.J.,
RA Chambers J.K., Szekeres P.G., Evans N.A., Schmidt D.B., Buckley P.T.,
RA Dytko G.M., Murdock P.R., Milligan G., Groarke D.A., Tan K.B.,
RA Shabon U., Nuthulaganti P., Wang D.Y., Wilson S., Bergsma D.J.,
RA Sarau H.M.;
RT "Receptor for the pain modulatory neuropeptides FF and AF is an orphan
RT G protein-coupled receptor.";

RL J. Biol. Chem. 275:25965-25971(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.
RC TISSUE=Spinal cord;
RX MEDLINE=20564301; PubMed=11024015;
RA Bonini J.A., Jones K.A., Adham N., Forray C., Artymyshyn R.,
RA Durkin M.M., Smith K.E., Tamm J.A., Boteju L.W., Lakhani P.P.,
RA Raddatz R., Yao W.-J., Ogozalek K.L., Boyle N., Kouranova E.V.,
RA Quan Y., Vaysse P.J., Wetzel J.M., Branchek T.A., Gerald C.,
RA Borowsky B.;
RT "Identification and characterization of two G protein-coupled
receptors for neuropeptide FF.";
RL J. Biol. Chem. 275:39324-39331(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=20299143; PubMed=10837915;
RA Parker R.M.C., Copeland N.G., Eyre H.J., Liu M., Gilbert D.J.,
RA Crawford J., Couzens M., Sutherland G.R., Jenkins N.A., Herzog H.;
RT "Molecular cloning and characterisation of GPR74 a novel G-protein
coupled receptor closest related to the Y-receptor family.";
RL Brain Res. Mol. Brain Res. 77:199-208(2000).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Liu Q., Guan X.-M., McDonald T.P., Jiang Q., Zeng Z., Marlene J.,
RA Williams D.L. Jr., Hong Y., Figueroa D., Clements M.K., Mallee J.,
RA Wang R., Evans J., Gould R., Austin C.P.;
RT "Identification and characterization of two cognate receptors for
RT mammalian FMRFamide-like neuropeptides.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RA Laemmle B.S., Schindler M., Beilmann M., Hamilton B.S., Doods H.N.,
RA Wieland H.A.;
RT "Cloning and characterization of the NPGP receptor and identification
RT of a novel short mRNA isoform in human hypothalamus.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Receptor for NPAF (A-18-F-amide) and NPFF (F-8-F-amide)
CC neuropeptides, also known as morphine-modulating peptides. Can
CC also be activated by a variety of naturally occurring or synthetic
CC FMRF-amide like ligands. This receptor mediates its action by
CC association with G proteins that activate a phosphatidylinositol-
CC calcium second messenger system.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=Experimental confirmation may be lacking for some
CC isoforms;
CC Name=1; Synonyms=long form;
CC IsoId=Q9Y5X5-1; Sequence=Displayed;
CC Name=2; Synonyms=short form;
CC IsoId=Q9Y5X5-2; Sequence=VSP_001907;
CC Name=3;
CC IsoId=Q9Y5X5-3; Sequence=VSP_001908, VSP_001909;
CC Name=4;
CC IsoId=Q9Y5X5-4; Sequence=VSP_001910, VSP_001911;
CC -!- TISSUE SPECIFICITY: Isoform 1 is abundant in placenta. Relatively
CC highly expressed in thymus, testis, and small intestine. Expressed
CC at low levels in several tissues including spleen, prostate,
CC brain, heart, ovary, colon, kidney, lung, liver and pancreas and
CC not expressed in skeletal muscle and leukocytes. Highest but
CC relatively low level of isoform 2 in placenta and very low level
CC in numerous tissues including adipose tissue and many brain
CC regions. Isoform 3 is expressed in brain and heart and, at lower
CC levels, in kidney, liver, lung and pancreas.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC HIGHEST TO OREXIN, NPY AND CHOLECYSTOKININ RECEPTORS.
CC -!- CAUTION: Ref.4 sequence differs from that shown due to a
CC frameshift in position 503.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC or send an email to license@isb-sib.ch).

CC -----
DR EMBL; AF119815; AAD22047.1; -.
DR EMBL; AF257210; AAF87078.1; -.
DR EMBL; AF268899; AAG41398.1; -.
DR EMBL; AF236083; AAK58513.1; ALT_FRAME.
DR EMBL; AF330053; AAK94197.1; -.
DR EMBL; AJ311393; CAC85427.1; -.
DR Genew; HGNC:4525; GPR74.
DR MIM; 607449; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
DR GO; GO:0008151; P:cell growth and/or maintenance; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR GO; GO:0009582; P:perception of abiotic stimulus; TAS.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR005395; NPFF_receptor.
DR InterPro; IPR005397; NPFF_receptor2.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PRINTS; PR01570; NPFFRECEPTOR.
DR PRINTS; PR01572; NPFFRECEPTR2.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Alternative splicing.
FT DOMAIN 1 147 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 148 168 1 (POTENTIAL).
FT DOMAIN 169 184 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 185 205 2 (POTENTIAL).
FT DOMAIN 206 221 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 222 242 3 (POTENTIAL).
FT DOMAIN 243 262 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 263 283 4 (POTENTIAL).
FT DOMAIN 284 319 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 320 340 5 (POTENTIAL).
FT DOMAIN 341 377 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 378 398 6 (POTENTIAL).
FT DOMAIN 399 413 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 414 434 7 (POTENTIAL).
FT DOMAIN 435 522 CYTOPLASMIC (POTENTIAL).
FT DISULFID 220 308 BY SIMILARITY.
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1 102 Missing (in isoform 2).
FT /FTId=VSP_001907.
FT VARSPLIC 1 99 Missing (in isoform 3).
FT /FTId=VSP_001908.
FT VARSPLIC 100 100 R -> M (in isoform 3).
FT /FTId=VSP_001909.
FT VARSPLIC 101 132 FIMNEKWDTNSSENWHPIWNVNDTKHHLYSDI -> MAIWK
FT HDVQDWIGPGNICRSFSLYVSCNCCR (in isoform
FT 4).
FT /FTId=VSP_001910.
FT VARSPLIC 133 522 Missing (in isoform 4).
FT /FTId=VSP_001911.
FT CONFLICT 466 466 A -> T (IN REF. 1 AND 4).
SQ SEQUENCE 522 AA; 60270 MW; 40CB9FCD42F77041 CRC64;

Query Match 100.0%; Score 2208; DB 1; Length 522;
Best Local Similarity 100.0%; Pred. No. 1.1e-136;
Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNEKWDTNSSENWHPIWNVNDTKHHLYSDINITYVNYYLHQPVAAIFIISYFLIFFLCM 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 103 MNEKWDTNSSENWHPIWNVNNDTKHHLYSDINITYVNYYLHQPVAAIFIISYFLIFFLCM 162
 Qy 61 MGNTVVCFIVMRNKHMHVTNLIFILNLAISDLLVGIFCMPITLLDNIIAGWPFGNTMCKI 120
 |||||||
 Db 163 MGNTVVCFIVMRNKHMHVTNLIFILNLAISDLLVGIFCMPITLLDNIIAGWPFGNTMCKI 222
 Qy 121 SGLVQGISVAASVFTLVAIAVDRFQCVVYPFKPKLTIKTAFVIIMIIWLAITIMSPSAV 180
 |||||||
 Db 223 SGLVQGISVAASVFTLVAIAVDRFQCVVYPFKPKLTIKTAFVIIMIIWLAITIMSPSAV 282
 Qy 181 MLHVQEEKYYRVRLNSQNKTSPVYWCREDWPNCMRKIYTTVLFANIYLAPLSLIVIMYG 240
 |||||||
 Db 283 MLHVQEEKYYRVRLNSQNKTSPVYWCREDWPNCMRKIYTTVLFANIYLAPLSLIVIMYG 342
 Qy 241 RIGISLFRAAVPHTGRKNQEWHVVSRRKKQKIIKMLLIVALLFILSWLPLWTLMMLSDYA 300
 |||||||
 Db 343 RIGISLFRAAVPHTGRKNQEWHVVSRRKKQKIIKMLLIVALLFILSWLPLWTLMMLSDYA 402
 Qy 301 DLSPNELQIINIYIYPFAHWAFLGNSSVNPIIYGFFNENFRRGFQEAFQLQLCQKRAKPM 360
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 Db 403 DLSPNELQIINIYIYPFAHWAFLGNSSVNPIIYGFFNENFRRGFQEAFQLQLCQKRAKPM 462
 Qy 361 EAYALKAKSHVLINTSNQLVQESTFQNPHGETLLYRKSAEKPQQELVMEELKETNSSEI 420
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 Db 463 EAYALKAKSHVLINTSNQLVQESTFQNPHGETLLYRKSAEKPQQELVMEELKETNSSEI 522

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	1748.5	79.2	417	11	Q924H0	Q924h0 mus musculu
2	1748.5	79.2	417	11	Q8BKR6	Q8bkr6 mus musculu
3	1666	75.5	405	11	Q924N0	Q924n0 mus musculu
4	984	44.6	432	11	Q924G9	Q924g9 rattus norv
5	553	25.0	758	5	Q7YU49	Q7yu49 drosophila
6	499.5	22.6	425	4	Q9HBV6	Q9hbv6 homo sapien
7	487.5	22.1	449	5	Q9VB87	Q9vb87 drosophila
8	487	22.1	422	11	Q8VHD7	Q8vhd7 rattus norv
9	486.5	22.0	365	11	Q8BHH0	Q8bhh0 mus musculu
10	485	22.0	600	5	Q9VW75	Q9vw75 drosophila
11	476	21.6	402	5	Q964E5	Q964e5 dugesia tig
12	470.5	21.3	429	5	P92045	P92045 lymnaea sta
13	469.5	21.3	364	11	Q8BV78	Q8bv78 mus musculu
14	463.5	21.0	381	11	Q8BWV1	Q8bwv1 mus musculu
15	460.5	20.9	381	11	Q9ERC0	Q9erc0 rattus norv
16	455.5	20.6	540	5	Q9VRM0	Q9vrm0 drosophila
17	451.5	20.4	375	13	057463	057463 brachydanio